



SEQUENCE LISTING

<110> Bayer Corporation

<120> Protein Having Activity As An Angiogenesis Modulator

<130> MSB-7265-PCT

<140> PCT/US 01/10222

<141> 2001-03-30

<150> US 60/266,300

<151> 2000-03-31

<160> 34

<170> PatentIn version 3.1

<210> 1

<211> 208

<212> PRT

<213> Homo sapiens

<400> 1

Gln Val His Gly Gly Phe Ser Gln Trp Ser Ala Trp Arg Ala Cys Ser
1 5 10 15

Val Thr Cys Gly Lys Gly Ile Gln Lys Arg Ser Arg Leu Cys Asn Gln
20 25 30

Pro Leu Pro Ala Asn Gly Gly Lys Pro Cys Gln Gly Ser Asp Leu Glu
35 40 45

Met Arg Asn Cys Gln Asn Lys Pro Cys Pro Val Asp Gly Ser Trp Ser
50 55 60

Glu Trp Ser Leu Trp Glu Glu Cys Thr Arg Ser Cys Gly Arg Gly Asn
65 70 75 80

Gln Thr Arg Thr Arg Thr Cys Asn Asn Pro Ser Val Gln His Gly Gly
85 90 95

Arg Pro Cys Glu Gly Asn Ala Val Glu Ile Ile Met Cys Asn Ile Arg
100 105 110

Pro Cys Pro Val His Gly Ala Trp Ser Ala Trp Gln Pro Trp Gly Thr
115 120 125

Cys Ser Glu Ser Cys Gly Lys Gly Thr Gln Thr Arg Ala Arg Leu Cys
130 135 140

Asn Asn Pro Pro Pro Ala Phe Gly Gly Ser Tyr Cys Asp Gly Ala Glu
145 150 155 160

Thr Gln Met Gln Val Cys Asn Glu Arg Asn Cys Pro Ile His Gly Lys
165 170 175

Trp Ala Thr Trp Ala Ser Trp Ser Ala Cys Ser Val Ser Cys Gly Gly
180 185 190

Gly Ala Arg Gln Arg Thr Arg Gly Cys Ser Asp Pro Val Pro Gln Tyr
195 200 205

<210> 2
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> Random sequence

<400> 2

Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Ala Asn Pro Gln Leu
1 5 10 15

Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu
20 25 30

Arg Asp Asn Gln Leu Val Val Glu Gly Leu Tyr Leu Ile Tyr Ser Gln
35 40 45

Val Leu Phe
50

<210> 3
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Random sequence

<400> 3

Arg Ala Pro Phe Lys Lys Ser Trp Ala Tyr Leu Gln Val Ala Lys His

1	5	10	15
Lys	Leu	Ser	Trp
Asn	Lys	Asp	Gly
Ile	Leu	His	Gly
Val	Arg	Tyr	Gln
20	25	30	
Asp	Gly	Asn	Leu
Val	Ile	Gln	Phe
Pro	Gly	Leu	Tyr
Phe	Ile	Ile	Cys
35	40	45	
Gln	Leu	Gln	Phe
50			

<210> 4
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FLAG sequence for expressed protein
 <400> 4

Asp	Tyr	Lys	Asp	Asp	Asp	Lys
1			5			

<210> 5
 <211> 6
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Sequence with antineoangiogenic activity
 <400> 5

Cys	Ser	Val	Thr	Cys	Gly
1				5	

<210> 6
 <211> 50
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Isolated type 1 thrombospondin domain sequence
 <400> 6

Asp	Gly	Trp	Ser	Pro	Trp	Ser	Glu	Trp	Thr	Ser	Cys	Ser	Thr	Ser	Cys
1				5				10						15	

Gly Asn Gly Ile Gln Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn
20 25 30

Arg Cys Glu Gly Ser Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu
35 40 45

Cys Asp
50

<210> 7
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Isolated type 1 thrombospondin domain sequence

<400> 7

Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser Val Thr Cys
1 5 10 15

Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser Pro Ser Pro
20 25 30

Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu Thr Lys Ala
35 40 45

Cys Lys Lys Asp Ala Cys Pro
50 55

<210> 8
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Isolated type 1 thrombospondin domain sequence

<400> 8

Gly Gly Trp Gly Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys
1 5 10 15

Gly Gly Gly Val Gln Lys Arg Ser Arg Leu Cys Asn Asn Pro Thr Pro
20 25 30

Gln Phe Gly Gly Lys Asp Cys Val Gly Asp Val Thr Glu Asn Gln Ile

35

40

45

Cys Asn Lys Gln Asp Cys Pro
50 55

<210> 9

<211> 50

<212> PRT

<213> Artificial Sequence

<220>

<223> Isolated type 1 thrombospondin domain sequence

<400> 9

Glu Gly Trp Ser Pro Trp Ala Glu Trp Thr Gln Cys Ser Val Thr Cys
1 5 10 15

Gly Ser Gly Thr Gln Gln Arg Gly Arg Ser Cys Asp Val Thr Ser Asn
20 25 30

Thr Cys Leu Gly Pro Ser Ile Gln Thr Arg Ala Cys Ser Leu Ser Lys
35 40 45

Cys Asp
50

<210> 10

<211> 55

<212> PRT

<213> Artificial Sequence

<220>

<223> Isolated type 1 thrombospondin domain sequence

<400> 10

Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser Val Thr Cys
1 5 10 15

Gly Val Gly Asn Ile Thr Arg Ile Arg Leu Cys Asn Ser Pro Val Pro
20 25 30

Gln Met Gly Gly Lys Asn Cys Lys Gly Ser Gly Arg Glu Thr Lys Ala
35 40 45

Cys Gln Gly Ala Pro Cys Pro
50 55

<210> 11
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Isolated type 1 thrombospondin sequence

<400> 11

Gly Arg Trp Ser Pro Trp Ser Pro Trp Ser Ala Cys Thr Val Thr Cys
1 5 10 15

Ala Gly Gly Ile Arg Glu Arg Thr Arg Val Cys Asn Ser Pro Glu Pro
20 25 30

Gln Tyr Gly Gly Lys Ala Cys Val Gly Asp Val Gln Glu Arg Gln Met
35 40 45

Cys Asn Lys Arg Ser Cys Pro
50 55

<210> 12
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<223> Isolated type 1 thrombospondin domain sequence

<400> 12

Gly Gly Trp Lys Leu Trp Ser Leu Trp Gly Glu Cys Thr Arg Asp Cys
1 5 10 15

Gly Gly Gly Leu Gln Thr Arg Thr Arg Thr Cys Leu Pro Ala Pro Gly
20 25 30

Val Glu Gly Gly Gly Cys Glu Gly Val Leu Glu Glu Gly Arg Gln Cys
35 40 45

Asn Arg Glu Ala Cys Gly
50

<210> 13
<211> 53
<212> PRT

<213> Artificial Sequence

<220>

<223> Isolated type 1 thrombospondin domain sequence

<400> 13

Pro Ala Ala Glu Glu Trp Ser Pro Trp Ser Val Cys Ser Ser Thr Cys
1 5 10 15

Gly Glu Gly Trp Gln Thr Arg Thr Arg Phe Cys Val Ser Ser Ser Tyr
20 25 30

Ser Thr Gln Cys Ser Gly Pro Leu Arg Glu Gln Arg Leu Cys Asn Asn
35 40 45

Ser Ala Val Cys Pro
50

<210> 14

<211> 53

<212> PRT

<213> Artificial Sequence

<220>

<223> Isolated type 1 thrombospondin domain sequence

<400> 14

Gly Ala Trp Asp Glu Trp Ser Pro Trp Ser Leu Cys Ser Ser Thr Cys
1 5 10 15

Gly Arg Gly Phe Arg Asp Arg Thr Arg Thr Cys Arg Pro Pro Gln Phe
20 25 30

Gly Gly Asn Pro Cys Glu Gly Pro Glu Lys Gln Thr Lys Phe Cys Asn
35 40 45

Ile Ala Leu Cys Pro
50

<210> 15

<211> 53

<212> PRT

<213> Artificial Sequence

<220>

<223> Isolated type 1 thrombospondin domain sequence

<400> 15

Gly Asn Trp Asn Glu Trp Ser Ser Trp Ser Ala Cys Ser Ala Ser Cys
1 5 10 15

Ser Gln Gly Arg Gln Gln Arg Thr Arg Glu Cys Asn Gly Pro Ser Tyr
20 25 30

Gly Gly Ala Glu Cys Gln Gly His Trp Val Glu Thr Arg Asp Cys Phe
35 40 45

Leu Gln Gln Cys Pro
50

<210> 16

<211> 53

<212> PRT

<213> Artificial Sequence

<220>

<223> Isolated type 1 thrombospondin domain sequence

<400> 16

Gly Lys Trp Gln Ala Trp Ala Ser Trp Gly Ser Cys Ser Val Thr Cys
1 5 10 15

Gly Ala Gly Ser Gln Arg Arg Glu Arg Val Cys Ser Gly Pro Phe Phe
20 25 30

Gly Gly Ala Ala Cys Gln Gly Pro Gln Asp Glu Tyr Arg Gln Cys Gly
35 40 45

Thr Gln Arg Cys Pro
50

<210> 17

<211> 53

<212> PRT

<213> Artificial Sequence

<220>

<223> Isolated type 1 thrombospondin domain sequence

<400> 17

Pro Ala Ala Glu Glu Trp Ser Pro Trp Ser Val Cys Ser Leu Thr Cys
1 5 10 15

Gly Gln Gly Leu Gln Val Arg Thr Arg Ser Cys Val Ser Ser Pro Tyr
20 25 30

Gly Thr Leu Cys Ser Gly Pro Leu Arg Glu Thr Arg Pro Cys Asn Asn
35 40 45

Ser Ala Thr Cys Pro
50

<210> 18
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Isolated type 1 thrombospondin domain sequence

<400> 18

Gly Val Trp Glu Glu Trp Gly Ser Trp Ser Leu Cys Ser Arg Ser Cys
1 5 10 15

Gly Arg Gly Ser Arg Ser Arg Met Arg Thr Cys Val Pro Pro Gln His
20 25 30

Gly Gly Lys Ala Cys Glu Gly Pro Glu Leu Gln Thr Lys Leu Cys Ser
35 40 45

Met Ala Ala Cys Pro
50

<210> 19
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Isolated type 1 thrombospondin domain sequence

<400> 19

Gly Gln Trp Leu Glu Trp Gly Pro Trp Gly Pro Cys Ser Thr Ser Cys
1 5 10 15

Ala Asn Gly Thr Gln Gln Arg Ser Arg Lys Cys Ser Val Ala Gly Pro
20 25 30

Ala Trp Ala Thr Cys Thr Gly Ala Leu Thr Asp Thr Arg Glu Cys Ser
35 40 45

Asn Leu Glu Cys Pro
50

<210> 20
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Isolated type 1 thrombospondin domain sequence

<400> 20

Ser Lys Trp Gly Pro Trp Asn Ala Trp Ser Leu Cys Ser Lys Thr Cys
1 5 10 15

Asp Thr Gly Trp Gln Arg Arg Phe Arg Met Cys Gln Ala Thr Gly Thr
20 25 30

Gln Gly Tyr Pro Cys Glu Gly Thr Gly Glu Glu Val Lys Pro Cys Ser
35 40 45

Glu Lys Arg Cys Pro
50

<210> 21
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Isolated type 1 thrombospondin domain sequence

<400> 21

Ser Gly Val Glu Glu Trp Ser Gln Trp Ser Thr Cys Ser Val Thr Cys
1 5 10 15

Gly Gln Gly Ser Gln Val Arg Thr Arg Thr Cys Val Ser Pro Tyr Gly
20 25 30

Thr His Cys Ser Gly Pro Leu Arg Glu Ser Arg Val Cys Asn Asn Thr
35 40 45

Ala Leu Cys Pro

50

<210> 22
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Isolated type 1 thrombospondin domain sequence

<400> 22

Gly Val Trp Glu Glu Trp Ser Pro Trp Ser Leu Cys Ser Phe Thr Cys
1 5 10 15

Gly Arg Gly Gln Arg Thr Arg Thr Arg Ser Cys Thr Pro Pro Gln Tyr
20 25 30

Gly Gly Arg Pro Cys Glu Gly Pro Glu Thr His His Lys Pro Cys Asn
35 40 45

Ile Ala Leu Cys Pro
50

<210> 23
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Isolated type 1 thrombospondin domain sequence

<400> 23

Gly Gln Trp Gln Glu Trp Ser Ser Trp Ser Gln Cys Ser Val Thr Cys
1 5 10 15

Ser Asn Gly Thr Gln Gln Arg Ser Arg Gln Cys Thr Ala Ala Ala His
20 25 30

Gly Gly Ser Glu Cys Arg Gly Pro Trp Ala Glu Ser Arg Glu Cys Tyr
35 40 45

Asn Pro Glu Cys Thr
50

<210> 24
<211> 53

<212> PRT
<213> Artificial Sequence

<220>
<223> Isolated type 1 thrombospondin domain sequence

<400> 24

Gly Gln Trp Asn Gln Trp Gly His Trp Ser Gly Cys Ser Lys Ser Cys
1 5 10 15

Asp Gly Gly Trp Glu Arg Arg Ile Arg Thr Cys Gln Gly Ala Val Ile
20 25 30

Thr Gly Gln Gln Cys Glu Gly Thr Gly Glu Glu Val Arg Arg Cys Ser
35 40 45

Glu Gln Arg Cys Pro
50

<210> 25
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Isolated type 1 thrombospondin domain sequence

<400> 25

Gly Gly Phe Ser Gln Trp Ser Ala Trp Arg Ala Cys Ser Val Thr Cys
1 5 10 15

Gly Lys Gly Ile Gln Lys Arg Ser Arg Leu Cys Asn Gln Pro Leu Pro
20 25 30

Ala Asn Gly Gly Lys Pro Cys Gln Gly Ser Asp Leu Glu Met Arg Asn
35 40 45

Cys Gln Asn Lys Pro Cys Pro
50 55

<210> 26
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Isolated type 1 thrombospondin domain sequence

<400> 26

Gly Ser Trp Ser Glu Trp Ser Leu Trp Glu Glu Cys Thr Arg Ser Cys
1 5 10 15

Gly Arg Gly Asn Gln Thr Arg Thr Arg Thr Cys Asn Asn Pro Ser Val
20 25 30

Gln His Gly Gly Arg Pro Cys Glu Gly Asn Ala Val Glu Ile Ile Met
35 40 45

Cys Asn Ile Arg Pro Cys Pro
50 55

<210> 27

<211> 55

<212> PRT

<213> Artificial Sequence

<220>

<223> Isolated type 1 thrombospondin domain sequence

<400> 27

Gly Ala Trp Ser Ala Trp Gln Pro Trp Gly Thr Cys Ser Glu Ser Cys
1 5 10 15

Gly Lys Gly Thr Gln Thr Arg Ala Arg Leu Cys Asn Asn Pro Pro Pro
20 25 30

Ala Phe Gly Gly Ser Tyr Cys Asp Gly Ala Glu Thr Gln Met Gln Val
35 40 45

Cys Asn Glu Arg Asn Cys Pro
50 55

<210> 28

<211> 55

<212> PRT

<213> Artificial Sequence

<220>

<223> Isolated type 1 thrombospondin domain sequence

<400> 28

Gly Lys Trp Ala Thr Trp Ala Ser Trp Ser Ala Cys Ser Val Ser Cys
1 5 10 15

Gly Gly Gly Ala Arg Gln Arg Thr Arg Gly Cys Ser Asp Pro Val Pro
20 25 30

Gln Tyr Gly Gly Arg Lys Cys Glu Gly Ser Asp Val Gln Ser Asp Phe
35 40 45

Cys Asn Ser Asp Pro Cys Pro
50 55

<210> 29
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Isolated type 1 thrombospondin domain sequence

<400> 29

Gly Asn Trp Ser Pro Trp Ser Gly Trp Gly Thr Cys Ser Arg Thr Cys
1 5 10 15

Asn Gly Gly Gln Met Arg Arg Tyr Arg Thr Cys Asp Asn Pro Pro Pro
20 25 30

Ser Asn Gly Gly Arg Ala Cys Gly Gly Pro Asp Ser Gln Ile Gln Arg
35 40 45

Cys Asn Thr Asp Met Cys Pro
50 55

<210> 30
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> Isolated type 1 thrombospondin domain sequence

<400> 30

Gly Ser Trp Gly Ser Trp His Ser Trp Ser Gln Cys Ser Ala Ser Cys
1 5 10 15

Gly Gly Gly Glu Lys Thr Arg Lys Arg Leu Cys Asp His Pro Val Pro
20 25 30

Val Lys Gly Gly Arg Pro Cys Pro Gly Asp Thr Thr Gln Val Thr Arg
 35 40 45

Cys Asn Val Gln Ala Cys Pro
 50 55

<210> 31
 <211> 197
 <212> PRT
 <213> Homo sapiens

<400> 31

Gln Trp Ser Ala Trp Arg Ala Cys Ser Val Thr Cys Gly Lys Gly Ile
 1 5 10 15

Gln Lys Arg Ser Arg Leu Cys Asn Gln Pro Leu Pro Ala Asn Gly Gly
 20 25 30

Lys Pro Cys Gln Gly Ser Asp Leu Glu Met Arg Asn Cys Gln Asn Lys
 35 40 45

Pro Cys Pro Val Asp Gly Ser Trp Ser Glu Trp Ser Leu Trp Glu Glu
 50 55 60

Cys Thr Arg Ser Cys Gly Arg Gly Asn Gln Thr Arg Thr Arg Thr Cys
 65 70 75 80

Asn Asn Pro Ser Val Gln His Gly Gly Arg Pro Cys Glu Gly Asn Ala
 85 90 95

Val Glu Ile Ile Met Cys Asn Ile Arg Pro Cys Pro Val His Gly Ala
 100 105 110

Trp Ser Ala Trp Gln Pro Trp Gly Thr Cys Ser Glu Ser Cys Gly Lys
 115 120 125

Gly Thr Gln Thr Arg Ala Arg Leu Cys Asn Asn Pro Pro Pro Ala Phe
 130 135 140

Gly Gly Ser Tyr Cys Asp Gly Ala Glu Thr Gln Met Gln Val Cys Asn
 145 150 155 160

Glu Arg Asn Cys Pro Ile His Gly Lys Trp Ala Thr Trp Ala Ser Trp

165

170

175

Ser Ala Cys Ser Val Ser Cys Gly Gly Gly Ala Arg Gln Arg Thr Arg
 180 185 190

Gly Cys Ser Asp Pro
 195

<210> 32
 <211> 194
 <212> PRT
 <213> Homo sapiens

<400> 32

Glu Trp Ser Pro Trp Ser Val Cys Ser Ser Thr Cys Gly Glu Gly Trp
 1 5 10 15

Gln Thr Arg Thr Arg Phe Cys Val Ser Ser Ser Tyr Ser Thr Gln Cys
 20 25 30

Ser Gly Pro Leu Arg Glu Gln Arg Leu Cys Asn Asn Ser Ala Val Cys
 35 40 45

Pro Val His Gly Ala Trp Asp Glu Trp Ser Pro Trp Ser Leu Cys Ser
 50 55 60

Ser Thr Cys Gly Arg Gly Phe Arg Asp Arg Thr Arg Thr Cys Arg Pro
 65 70 75 80

Pro Gln Phe Gly Gly Asn Pro Cys Glu Gly Pro Glu Lys Gln Thr Lys
 85 90 95

Phe Cys Asn Ile Ala Leu Cys Pro Gly Arg Ala Val Asp Gly Asn Trp
 100 105 110

Asn Glu Trp Ser Ser Trp Ser Ala Cys Ser Ala Ser Cys Ser Gln Gly
 115 120 125

Arg Gln Gln Arg Thr Arg Glu Cys Asn Gly Pro Ser Tyr Gly Gly Ala
 130 135 140

Glu Cys Gln Gly His Trp Val Glu Thr Arg Asp Cys Phe Leu Gln Gln
 145 150 155 160

Cys Pro Val Asp Gly Lys Trp Gln Ala Trp Ala Ser Trp Gly Ser Cys
165 170 175

Ser Val Thr Cys Gly Ala Gly Ser Gln Arg Arg Glu Arg Val Cys Ser
180 185 190

Gly Pro

<210> 33
<211> 1336
<212> PRT
<213> Homo sapiens

<400> 33

Thr Pro Ile Gly Arg Pro Arg Ile Arg His Gln Asp Lys Arg Thr Val
1 5 10 15

Asp Leu Thr Val Gln Val Pro Pro Ser Ile Ala Asp Glu Pro Thr Asp
20 25 30

Phe Leu Val Thr Lys His Ala Pro Ala Val Ile Thr Cys Thr Ala Ser
35 40 45

Gly Val Pro Phe Pro Ser Ile His Trp Thr Lys Asn Gly Ile Arg Leu
50 55 60

Leu Pro Arg Gly Asp Gly Tyr Arg Ile Leu Ser Ser Gly Ala Ile Glu
65 70 75 80

Ile Leu Ala Thr Gln Leu Asn His Ala Gly Arg Tyr Thr Cys Val Ala
85 90 95

Arg Asn Ala Ala Gly Ser Ala His Arg His Val Thr Leu His Val His
100 105 110

Glu Pro Pro Val Ile Gln Pro Gln Pro Ser Glu Leu His Val Ile Leu
115 120 125

Asn Asn Pro Ile Leu Leu Pro Cys Glu Ala Thr Gly Thr Pro Ser Pro
130 135 140

Phe Ile Thr Trp Gln Lys Glu Gly Ile Asn Val Asn Thr Ser Gly Arg

145		150		155		160
Asn His Ala Val	Leu Pro Ser Gly Gly	Leu Gln Ile Ser Arg Ala Val				
	165	170			175	
Arg Glu Asp Ala Gly Thr Tyr Met Cys Val Ala Gln Asn Pro Ala Gly						
	180	185			190	
Thr Ala Leu Gly Lys Ile Lys Leu Asn Val Gln Val Pro Pro Val Ile						
	195	200			205	
Ser Pro His Leu Lys Glu Tyr Val Ile Ala Val Asp Lys Pro Ile Thr						
	210	215			220	
Leu Ser Cys Glu Ala Asp Gly Leu Pro Pro Pro Asp Ile Thr Trp His						
	225	230			235	240
Lys Asp Gly Arg Ala Ile Val Glu Ser Ile Arg Gln Arg Val Leu Ser						
	245	250			255	
Ser Gly Ser Leu Gln Ile Ala Phe Val Gln Pro Gly Asp Ala Gly His						
	260	265			270	
Tyr Thr Cys Met Ala Ala Asn Val Ala Gly Ser Ser Ser Thr Ser Thr						
	275	280			285	
Lys Leu Thr Val His Val Pro Pro Arg Ile Arg Ser Thr Lys Gly His						
	290	295			300	
Tyr Thr Val Asn Glu Asn Ser Gln Ala Ile Leu Pro Cys Val Ala Asp						
	305	310			315	320
Gly Ile Pro Thr Pro Ala Ile Asn Trp Lys Lys Asp Asn Val Leu Leu						
	325	330			335	
Ala Asn Leu Leu Gly Lys Tyr Thr Ala Glu Pro Tyr Gly Glu Leu Ile						
	340	345			350	
Leu Glu Asn Val Val Leu Glu Asp Ser Gly Phe Tyr Thr Cys Val Ala						
	355	360			365	
Asn Asn Ala Ala Gly Glu Asp Thr His Thr Val Ser Leu Thr Val His						
	370	375			380	

Val Leu Pro Thr Phe Thr Glu Leu Pro Gly Asp Val Ser Leu Asn Lys
385 390 395 400

Gly Glu Gln Leu Arg Leu Ser Cys Lys Ala Thr Gly Ile Pro Leu Pro
405 410 415

Lys Leu Thr Trp Thr Phe Asn Asn Asn Ile Ile Pro Ala His Phe Asp
420 425 430

Ser Val Asn Gly His Ser Glu Leu Val Ile Glu Arg Val Ser Lys Glu
435 440 445

Asp Ser Gly Thr Tyr Val Cys Thr Ala Glu Asn Ser Val Gly Phe Val
450 455 460

Lys Ala Ile Gly Phe Val Tyr Val Lys Glu Pro Pro Val Phe Lys Gly
465 470 475 480

Asp Tyr Pro Ser Asn Trp Ile Glu Pro Leu Gly Gly Asn Ala Ile Leu
485 490 495

Asn Cys Glu Val Lys Gly Asp Pro Thr Pro Thr Ile Gln Trp Asn Arg
500 505 510

Lys Gly Val Asp Ile Glu Ile Ser His Arg Ile Arg Gln Leu Gly Asn
515 520 525

Gly Ser Leu Ala Ile Tyr Gly Thr Val Asn Glu Asp Ala Gly Asp Tyr
530 535 540

Thr Cys Val Ala Thr Asn Glu Ala Gly Val Val Glu Arg Ser Met Ser
545 550 555 560

Leu Thr Leu Arg Ser Pro Pro Ile Ile Thr Leu Glu Pro Val Glu Thr
565 570 575

Val Ile Asn Ala Gly Gly Lys Ile Ile Leu Asn Cys Gln Ala Thr Gly
580 585 590

Glu Pro Gln Pro Thr Ile Thr Trp Ser Arg Gln Gly His Ser Ile Ser
595 600 605

Trp Asp Asp Arg Val Asn Val Leu Ser Asn Asn Ser Leu Tyr Ile Ala
610 615 620

Asp Ala Gln Lys Glu Asp Thr Ser Glu Phe Glu Cys Val Ala Arg Asn
625 630 635 640

Leu Met Gly Ser Val Leu Val Arg Val Pro Val Ile Val Gln Val His
645 650 655

Gly Gly Phe Ser Gln Trp Ser Ala Trp Arg Ala Cys Ser Val Thr Cys
660 665 670

Gly Lys Gly Ile Gln Lys Arg Ser Arg Leu Cys Asn Gln Pro Leu Pro
675 680 685

Ala Asn Gly Gly Lys Pro Cys Gln Gly Ser Asp Leu Glu Met Arg Asn
690 695 700

Cys Gln Asn Lys Pro Cys Pro Val Asp Gly Ser Trp Ser Glu Trp Ser
705 710 715 720

Leu Trp Glu Glu Cys Thr Arg Ser Cys Gly Arg Gly Asn Gln Thr Arg
725 730 735

Thr Arg Thr Cys Asn Asn Pro Ser Val Gln His Gly Gly Arg Pro Cys
740 745 750

Glu Gly Asn Ala Val Glu Ile Ile Met Cys Asn Ile Arg Pro Cys Pro
755 760 765

Val His Gly Ala Trp Ser Ala Trp Gln Pro Trp Gly Thr Cys Ser Glu
770 775 780

Ser Cys Gly Lys Gly Thr Gln Thr Arg Ala Arg Leu Cys Asn Asn Pro
785 790 795 800

Pro Pro Ala Phe Gly Gly Ser Tyr Cys Asp Gly Ala Glu Thr Gln Met
805 810 815

Gln Val Cys Asn Glu Arg Asn Cys Pro Ile His Gly Lys Trp Ala Thr
820 825 830

Trp Ala Ser Trp Ser Ala Cys Ser Val Ser Cys Gly Gly Gly Ala Arg
835 840 845

Gln Arg Thr Arg Gly Cys Ser Asp Pro Val Pro Gln Tyr Gly Gly Arg
850 855 860

Lys Cys Glu Gly Ser Asp Val Gln Ser Asp Phe Cys Asn Ser Asp Pro
865 870 875 880

Cys Pro Thr His Gly Asn Trp Ser Pro Trp Ser Gly Trp Gly Thr Cys
885 890 895

Ser Arg Thr Cys Asn Gly Gly Gln Met Arg Arg Tyr Arg Thr Cys Asp
900 905 910

Asn Pro Pro Pro Ser Asn Gly Gly Arg Ala Cys Gly Gly Pro Asp Ser
915 920 925

Gln Ile Gln Arg Cys Asn Thr Asp Met Cys Pro Val Asp Gly Ser Trp
930 935 940

Gly Ser Trp His Ser Trp Ser Gln Cys Ser Ala Ser Cys Gly Gly Gly
945 950 955 960

Glu Lys Thr Arg Lys Arg Leu Cys Asp His Pro Val Pro Val Lys Gly
965 970 975

Gly Arg Pro Cys Pro Gly Asp Thr Thr Gln Val Thr Arg Cys Asn Val
980 985 990

Gln Ala Cys Pro Gly Gly Pro Gln Arg Ala Arg Gly Ser Val Ile Gly
995 1000 1005

Asn Ile Asn Asp Val Glu Phe Gly Ile Ala Phe Leu Asn Ala Thr
1010 1015 1020

Ile Thr Asp Ser Pro Asn Ser Asp Thr Arg Ile Ile Arg Ala Lys
1025 1030 1035

Ile Thr Asn Val Pro Arg Ser Leu Gly Ser Ala Met Arg Lys Ile
1040 1045 1050

Val Ser Ile Leu Asn Pro Ile Tyr Trp Thr Thr Ala Lys Glu Ile

1055	1060	1065
Gly Glu Ala Val Asn Gly Phe Thr Leu Thr Asn Ala Val Phe Lys 1070 1075 1080		
Arg Glu Thr Gln Val Glu Phe Ala Thr Gly Glu Ile Leu Gln Met 1085 1090 1095		
Ser His Ile Ala Arg Gly Leu Asp Ser Asp Gly Ser Leu Leu Leu 1100 1105 1110		
Asp Ile Val Val Ser Gly Tyr Val Leu Gln Leu Gln Ser Pro Ala 1115 1120 1125		
Glu Val Thr Val Lys Asp Tyr Thr Glu Asp Tyr Ile Gln Thr Gly 1130 1135 1140		
Pro Gly Gln Leu Tyr Ala Tyr Ser Thr Arg Leu Phe Thr Ile Asp 1145 1150 1155		
Gly Ile Ser Ile Pro Tyr Thr Trp Asn His Thr Val Phe Tyr Asp 1160 1165 1170		
Gln Ala Gln Gly Arg Met Pro Phe Leu Val Glu Thr Leu His Ala 1175 1180 1185		
Ser Ser Val Glu Ser Asp Tyr Asn Gln Ile Glu Glu Thr Leu Gly 1190 1195 1200		
Phe Lys Ile His Ala Ser Ile Ser Lys Gly Asp Arg Ser Asn Gln 1205 1210 1215		
Cys Pro Ser Gly Phe Thr Leu Asp Ser Val Gly Pro Phe Cys Ala 1220 1225 1230		
Asp Glu Asp Glu Cys Ala Ala Gly Asn Pro Cys Ser His Ser Cys 1235 1240 1245		
His Asn Ala Met Gly Thr Tyr Tyr Cys Ser Cys Pro Lys Gly Leu 1250 1255 1260		
Thr Ile Ala Ala Asp Gly Arg Thr Cys Gln Asp Ile Asp Glu Cys 1265 1270 1275		

Ala Leu Gly Arg His Thr Cys His Ala Gly Gln Asp Cys Asp Asn
 1280 1285 1290

Thr Ile Gly Ser Tyr Arg Cys Val Val Arg Cys Gly Ser Gly Phe
 1295 1300 1305

Arg Arg Thr Ser Asp Gly Leu Ser Cys Gln Asp Ile Asn Glu Cys
 1310 1315 1320

Gln Glu Ser Ser Pro Val Thr Ser Ala Val Ser Met Pro
 1325 1330 1335

<210> 34
 <211> 4073
 <212> DNA
 <213> Homo sapiens

<400> 34
 actcctatag ggcggccgcg aattcggcac caggataaaa gaactgtgga tctcactgtc 60
 caagttccac cttccatagc tgatgagcct acagatttcc tagtaaccaa acatgccccca 120
 gcagtaatta cctgcactgc ttcgggaggt ccatttccct caattcactg gaccaaaaat 180
 ggtataagac tgcttcccag gggagatggc tatagaattc tgtcctcagg agcaattgaa 240
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